SEQUENCE LISTING

<110> Chang, Tai-Jay

<120> ANDROGEN RECEPTOR COMPLEX-ASSOCIATED PROTEIN

<130> 11709-003001

<140> US 09/781,693

<141> 2001-02-12

<150> US 60/262,312

<151> 2001-01-17

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aatgaaaata acaccaatcc tgagcctcag ttccaaacag aagccactgg gccttcagct 1920 1980 catgaagaaa catccaccag ggactctgct cttcaggaca cagatgacag tgatgatgac ccagtcctga tcccaggtgc aaggtatcga gcaggacctg gtgatagacg ctctgctgtt 2040 qcccgtattc aggagttctt cagacggaga aaagaaagga aagaaatgga agaattggat 2100 actttgaaca ttagaaggcc gctagtaaaa atggtttata aaggccatcg caactccagg 2160 acaatgataa aagaagccaa tttctggggt gctaactttg taatgagtgg ttctgactgt 2220 qqccacattt tcatctggga tcggcacact gctgagcatt tgatgcttct ggaagctgat 2280 aatcatgtgg taaactgcct gcagccacat ccgtttgacc caattttagc ctcatctggc 2340 2400 atagattatg acataaagat ctggtcacca ttagaagagt caaggatttt taaccgaaaa cttgctgatg aagttataac tcgaaacgaa ctcatgctgg aagaaactag aaacaccatt 2460 2520 acagttccag cctctttcat gttgaggatg ttggcttcac ttaatcatat ccgagctgac 2580 cggttggagg gtgacagatc agaaggctct ggtcaagaga atgaaaatga ggatgaggaa

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a' wit

Pro Pro Val Lys Arg Leu Arg Leu Arg Gly Asp Trp Ser Asp Thr Gly Pro Arg Ala Arg Pro Glu Ser Glu Arg Glu Arg Asp Gly Glu Gln Ser Pro Asn Val Ser Leu Met Gln Arg Met Ser Asp Met Leu Ser Arg Trp Phe Glu Glu Ala Ser Glu Val Ala Gln Ser Asn Arg Gly Arg Gly Arg Ser Arg Pro Arg Gly Gly Thr Ser Gln Ser Asp Ile Ser Thr Leu Pro Thr Val Pro Ser Ser Pro Asp Leu Glu Val Ser Glu Thr Ala Met Glu Val Asp Thr Pro Ala Glu Gln Phe Leu Gln Pro Ser Thr Ser Ser Thr Met Ser Ala Gln Ala His Ser Thr Ser Ser Pro Thr Glu Ser Pro His Ser Thr Pro Leu Leu Ser Ser Pro Asp Ser Glu Gln Arg Gln Ser Val Glu Ala Ser Gly His His Thr His His Gln Ser Asp Asn Asn Glu Lys Leu Ser Pro Lys Pro Gly Thr Gly Glu Pro Val Leu Ser Leu His Tyr Ser Thr Glu Gly Thr Thr Thr Ser Thr Ile Lys Leu Asn Phe Thr Asp Glu Trp Ser Ser Ile Ala Ser Ser Ser Arg Gly Ile Gly Ser His Cys Lys Ser Glu Gly Gln Glu Glu Ser Phe Val Pro Gln Ser Ser Val Gln Pro Pro Glu Gly Asp Ser Glu Thr Lys Ala Pro Glu Glu Ser Ser Glu Asp Val Thr Lys Tyr Gln Glu Gly Val Ser Ala Glu Asn Pro Val Glu Asn His Ile Asn Ile Thr Gln Ser Asp Lys Phe Thr Ala Lys Pro Leu Asp Ser Asn Ser Gly Glu Arg Asn Asp Leu Asn Leu Asp Arg Ser Cys Gly Val Pro Glu Glu Ser Ala Ser Ser Glu Lys Ala Lys Glu Pro Glu Thr Ser Asp Gln Thr Ser Thr Glu Ser Ala Thr Asn Glu Asn Asn Thr Asn Pro Glu Pro Gln Phe Gln Thr Glu Ala Thr Gly Pro Ser Ala His Glu Glu Thr Ser Thr Arg Asp Ser Ala Leu Gln Asp Thr Asp Asp Ser Asp Asp Asp Pro Val Leu Ile Pro Gly Ala Arg Tyr Arg Ala Gly Pro Gly Asp Arg Arg Ser Ala Val Ala Arg Ile Gln Glu Phe Phe Arg Arg Arg Lys Glu Arg Lys Glu Met Glu Glu Leu Asp Thr Leu Asn Ile Arg Arg Pro Leu Val Lys Met Val Tyr Lys Gly His Arg Asn Ser Arg Thr Met Ile Lys Glu Ala Asn Phe Trp Gly Ala Asn Phe Val Met Ser Gly Ser Asp Cys Gly His Ile Phe Ile Trp Asp Arg His Thr Ala Glu His Leu Met Leu Leu Glu Ala Asp Asn His Val Val Asn Cys Leu Gln

al Contr

760 755 Pro His Pro Phe Asp Pro Ile Leu Ala Ser Ser Gly Ile Asp Tyr Asp 780 775 Ile Lys Ile Trp Ser Pro Leu Glu Glu Ser Arg Ile Phe Asn Arg Lys 795 790 Leu Ala Asp Glu Val Ile Thr Arg Asn Glu Leu Met Leu Glu Glu Thr 810 805 Arg Asn Thr Ile Thr Val Pro Ala Ser Phe Met Leu Arg Met Leu Ala 830 825 Ser Leu Asn His Ile Arg Ala Asp Arg Leu Glu Gly Asp Arg Ser Glu 840 Gly Ser Gly Gln Glu Asn Glu Asn Glu Asp Glu Glu 855 <210> 3 <211> 3016 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (18)...(2597) 50 ceggeteagg cagagee atg tet egg ggt gge tee tae eea cae etg ttg Met Ser Arg Gly Gly Ser Tyr Pro His Leu Leu tgg gac gtg agg aaa agg tcc ctc ggg ctg gag gac ccg tcc cgg ctg 98 Trp Asp Val Arg Lys Arg Ser Leu Gly Leu Glu Asp Pro Ser Arg Leu 146 cgg agt cgc tac ctg gga aga aga gaa ttt atc caa aga tta aaa ctt Arg Ser Arg Tyr Leu Gly Arg Arg Glu Phe Ile Gln Arg Leu Lys Leu 194 gaa gca acc ctt aat gtg cat gat ggt tgt gtt aat aca atc tgt tgg Glu Ala Thr Leu Asn Val His Asp Gly Cys Val Asn Thr Ile Cys Trp 45 aat gac act gga gaa tat att tta tct ggc tca gat gac acc aaa tta 242 Asn Asp Thr Gly Glu Tyr Ile Leu Ser Gly Ser Asp Asp Thr Lys Leu 60 65 gta att agt aat cct tac agc aga aag gtt ttg aca aca att cgt tca 290 Val Ile Ser Asn Pro Tyr Ser Arg Lys Val Leu Thr Thr Ile Arg Ser 80 90 338 ggg cac cga gca aac ata ttt agt gca aag ttc tta cct tgt aca aat Gly His Arg Ala Asn Ile Phe Ser Ala Lys Phe Leu Pro Cys Thr Asn 95 386 gat aaa cag att gta tee tge tet gga gat gga gta ata ttt tat acc Asp Lys Gln Ile Val Ser Cys Ser Gly Asp Gly Val Ile Phe Tyr Thr 110 434 aac gtt gag caa gat gca gaa acc aac aga caa tgc caa ttt acg tgt

ary.

	•																
Asn	Val 125	Glu	Gln	Asp	Ala	Glu 130	Thr	Asn	Arg	Gln	Cys 135	Gln	Phe	Thr	Cys		
cat His 140	tat Tyr	gga Gly	act Thr	act Thr	tat Tyr 145	gag Glu	att Ile	atg Met	act Thr	gta Val 150	ccc Pro	aat Asn	gac Asp	cct Pro	tac Tyr 155	482	
act Thr	ttt Phe	ctc Leu	tct Ser	tgt Cys 160	ggt Gly	gaa Glu	gat Asp	gga Gly	act Thr 165	gtt Val	agg Arg	tgg Trp	ttt Phe	gat Asp 170	aca Thr	530	
cgc Arg	atc Ile	aaa Lys	act Thr 175	agc Ser	tgc Cys	aca Thr	aaa Lys	gaa Glu 180	gat Asp	tgt Cys	aaa Lys	gat Asp	gat Asp 185	att Ile	tta Leu	578	
att Ile	aac Asn	tgt Cys 190	cga Arg	cgt Arg	gct Ala	gcc Ala	acg Thr 195	tct Ser	gtt Val	gct Ala	att Ile	tgc Cys 200	cca Pro	cca Pro	ata Ile	626	
cca Pro	tat Tyr 205	tac Tyr	ctt Leu	gct Ala	gtt Val	ggt Gly 210	tgt Cys	tct Ser	gac Asp	agc Ser	tca Ser 215	gta Val	cga Arg	ata Ile	tat Tyr	674	:
gat Asp 220	cgg Arg	cga Arg	atg Met	ctg Leu	ggc Gly 225	aca Thr	aga Arg	gct Ala	aca Thr	ggg Gly 230	aat Asn	tat Tyr	gca Ala	ggt Gly	cga Arg 235	722	!
gjå aaa	act Thr	act Thr	gga Gly	atg Met 240	gtt Val	gcc Ala	cgt Arg	ttt Phe	att Ile 245	cct Pro	tcc Ser	cat His	ctt Leu	aat Asn 250	aat Asn	770)
aag Lys	tcc Ser	tgc Cys	aga Arg 255	gtg Val	aca Thr	tct Ser	ctg Leu	tgt Cys 260	tac Tyr	agt Ser	gaa Glu	gat Asp	ggt Gly 265	caa Gln	gag Glu	818	}
att Ile	ctc Leu	gtt Val 270	agt Ser	tac Tyr	tct Ser	tca Ser	gat Asp 275	tac Tyr	ata Ile	tat Tyr	ctt Leu	ttt Phe 280	gac Asp	ccg Pro	aaa Lys	866	;
gat Asp	gat Asp 285	aca Thr	gca Ala	cga Arg	gaa Glu	ctt Leu 290	aaa Lys	act Thr	cct Pro	tct Ser	gcg Ala 295	gaa Glu	gag Glu	aga Arg	aga Arg	914	F
gaa Glu 300	gag Glu	ttg Leu	cga Arg	caa Gln	cca Pro 305	cca Pro	gtt Val	aag Lys	cgt Arg	ttg Leu 310	aga Arg	ctt Leu	cgt Arg	ggt Gly	gat Asp 315	962	2
tgg Trp	tca Ser	gat Asp	act Thr	gga Gly 320	Pro	aga Arg	gca Ala	agg Arg	ccg Pro 325	gag Glu	agt Ser	gaa Glu	cga Arg	gaa Glu 330	Arg	1010	כ
gat Asp	gga Gly	gag Glu	cag Gln 335	Ser	ccc Pro	aat Asn	gtg Val	tca Ser 340		atg Met	cag Gln	aga Arg	atg Met 345	Ser	gat Asp	105	3
atg Met	tta Leu	tca Ser	aga Arg	tgg Trp	ttt Phe	gaa Glu	gaa Glu	gca Ala	agt Ser	gag Glu	gtt Val	gca Ala	caa Gln	agc Ser	aat Asn	110	б

Ord Ord 350 355 360

		350					355					360				
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gaa Glu	act Thr	gca Ala	atg Met	gaa Glu 400	gta Val	gat Asp	act Thr	cca Pro	gct Ala 405	gaa Glu	caa Gln	ttt Phe	ctt Leu	cag Gln 410	cct Pro	1250
										cat His						1298
										tct Ser						1346
Gln	Arg 445	Gln	Ser	Val	Glu	Ala 450	Ser	Gly	His	cac His	Thr 455	His	His	Gln	Ser	1394
Asp 460	Asn	Asn	Asn	Glu	Lys 465	Leu	Ser	Pro	Lys	cca Pro 470	Gly	Thr	Gly	Glu	Pro 475	1442
Val	Leu	Ser	Leu	His 480	Tyr	Ser	Thr	Glu	Gly 485	aca Thr	Thr	Thr	Ser	Thr 490	Ile	1490
Lys	Leu	Asn	Phe 495	Thr	Asp	Glu	Trp	Ser 500	Ser	ata Ile	Ala	Ser	Ser 505	Ser	Arg	1538
Gly	Ile	Gly 510	Ser	His	Cys	Lys	Ser 515	Glu	Gly	çag Gln	Glu	Glu 520	Ser	Phe	Val	1586
Pro	Gln 525	Ser	Ser	Val	Gln	Pro 530	Pro	Glu	Gly	gac Asp	Ser 535	Glu	Thr	Lys	Ala	1634
Pro 540	Glu	Glu	Ser	Ser	Glu 545	Asp	Val	Thr	Lys	tat Tyr 550	Gln	Glu	Gly	Val	Ser 555	1682
Āla	Glu	Asn	Pro	Val 560	Glu	Asn	His	Ile	Asn 565	ata Ile	Thr	Gln	Ser	Asp 570	Lys	1730
										gga Gly						1778

Out.

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aaa Lys	gcc Ala 605	aag Lys	gaa Glu	cca Pro	gaa Glu	act Thr 610	tca Ser	gat Asp	cag Gln	act Thr	agc Ser 615	act Thr	gag Glu	agt Ser	gct Ala	1874
acc Thr 620	aat Asn	gaa Glu	aat Asn	aac Asn	acc Thr 625	aat Asn	cct Pro	gag Glu	cct Pro	cag Gln 630	ttc Phe	caa Gln	aca Thr	gaa Glu	gcc Ala 635	1922
act Thr	gly ggg	cct Pro	tca Ser	gct Ala 640	cat His	gaa Glu	gaa Glu	aca Thr	tcc Ser 645	acc Thr	agg Arg	gac Asp	tct Ser	gct Ala 650	ctt Leu	1970
cag Gln	gac Asp	aca Thr	gat Asp 655	gac Asp	agt Ser	gat Asp	gat Asp	gac Asp 660	cca Pro	gtc Val	ctg Leu	atc Ile	cca Pro 665	ggt Gly	gca Ala	2018
agg Arg	tat Tyr	cga Arg 670	gca Ala	gga Gly	cct Pro	ggt Gly	gat Asp 675	aga Arg	cgc Arg	tct Ser	gct Ala	gtt Val 680	gcc Ala	cgt Arg	att Ile	2066
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gat Asp 700	act Thr	ttg Leu	aac Asn	att Ile	aga Arg 705	agg Arg	ccg Pro	cta Leu	gta Val	aaa Lys 710	atg Met	gtt Val	tat Tyr	aaa Lys	ggc Gly 715	2162
cat His	cgc Arg	aac Asn	tcc Ser	agg Arg 720	Thr	atg Met	ata Ile	aaa Lys	gaa Glu 725	Ala	aat Asn	ttc Phe	tgg Trp	ggt Gly 730	Ala	2210
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cgg Arg	cac His	act Thr	Ala	gag Glu	cat His	ttg Leu	atg Met 755	Leu	ctg Leu	gaa Glu	gct Ala	gat Asp 760	Asn	cat His	gtg Val	2306
gta Val	aac Asn 765	суя	ctg Leu	cag Gln	cca Pro	cat His	Pro	ttt Phe	gac Asp	c cca pro	att 116 775	е ьеч	gco Ala	tca Ser	tct Ser	2354
ggc Gl _y 780	ıle	gat Asp	tat Tyr	gac Asp	ata Ile 785	Lys	ato Ile	tgg Tr	g tca p Sei	a cca Pro 790	ь гел	a gaa ı Glu	ı gagı ı Glu	tca Sei	a agg Arg 795	2402
att Ile	ttt Phe	aac Ası	c cga n Arg	aaa Lys 800	Let	gct Ala	; gat a Asp	gaa Gli	a gtt u Val 809	l Ile	a act	t cga r Arg	a aac g Asr	gaa Glu 810	a ctc 1 Leu)	2450

ant cont

•	
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ttg agg atg ttg gct tca ctt aat cat atc cga gct gac cgg ttg gag Leu Arg Met Leu Ala Ser Leu Asn His Ile Arg Ala Asp Arg Leu Glu 830 835 840	2546
ggt gac aga tca gaa ggc tct ggt caa gag aat gaa aat gag gat gag Gly Asp Arg Ser Glu Gly Ser Gly Gln Glu Asn Glu Asn Glu Asp Glu 845 850 855	2594
gaa taataaactc tttttggcaa gcacttaaat gttctgaaat ttgtataaga Glu 860	2647
catttattat attttttct ttacagagct ttagtgcaat tttaaggtta tggtttttgg agtttttccc tttttttggg ataacctaac attggtttgg aatgattgtg tgcatgaatt tgggagattg tataaaacaa aactagcaga atgtttttaa aactttttgc cgtgtatgag gagtgctaga aaatgcaaag tgcaatattt tccctaacct tcaaatgtgg gagcttggat caatgttgaa gaataatttt catcatagtg aaaatgttgg ttcaaataaa tttctacact tgccatttgc atgtttgttg ctttctaatt aaagaaactg gttgttttaa aaaaaaaaaa	2707 2767 2827 2887 2947 3007 3016
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Chy Chy

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Ond

<213> Artificial Sequence

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Control

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a